

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listing, of claims in the application:

1. (previously presented) A recombinant expression system comprising a host cell comprising a nucleic acid encoding a phytase enzyme (i) having the amino acid sequence as set forth in SEQ ID NO:2, or (ii) having an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, wherein the nucleic acid is operably linked to a transcription control sequence.

2. (currently amended) A vector comprising a nucleic acid (i) comprising a nucleotide sequence as set forth in SEQ ID NO:1, (ii) comprising a nucleotide sequence as set forth in SEQ ID NO:1 from nucleotide residue 1 to 1296, [(ii)] (iii) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2, or (iv) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, ~~or, (iii) encoding a phytase comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, wherein the phytase sequence has at least one conservative amino acid substitution, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, (f) a replacement among the aromatic residues Phe, Tyr, (g) any combination of a, b, c, d, e or f, or (iv) encoding a phytase comprising an enzymatically active fragment of (i), (ii) or (iii).~~

3. (previously presented) The expression system of claim 1 wherein the transcription control sequence comprises a constitutive promoter.

4. (previously presented) The expression system of claim 1 wherein the transcription

control sequence comprises a tissue-specific promoter.

5. (previously presented) The expression system of claim 1 wherein said host cell is a prokaryotic cell.

6. (previously presented) The expression system of claim 1 wherein said host cell is a eukaryotic cell.

7. (previously presented) The expression system of claim 1 wherein said host cell is a plant cell.

8. (previously presented) The expression system of claim 1 wherein the nucleic acid further comprises a sequence encoding a signal peptide or a transit peptide.

9. (previously presented) The expression system of claim 8 wherein said signal peptide is a pathogenesis-related (PR) protein PR-S signal peptide from tobacco.

10. (currently amended) A prokaryotic cell comprising an exogenous nucleic acid encoding a phytase enzyme, wherein the nucleic acid is operably linked to a transcriptional control sequence and the phytase enzyme (i) is encoded by a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, (ii) is encoded by a nucleic acid comprising a sequence as set forth in SEQ ID NO:1 from nucleotide residue 1 to 1296, [(ii)] (iii) comprises an amino acid sequence as set forth in SEQ ID NO:2, or (iv) comprises an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, ~~or, (iii) comprises an amino acid sequence as set forth in SEQ ID NO:2 or an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, having at least one conservative amino acid substitution, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic~~

~~residues Lys and Arg, (f) a replacement among the aromatic residues Phe, Tyr, or (g) any combination of a, b, c, d, e or f, or (iv) encoding a phytase comprising an enzymatically active fragment of (i), (ii) or (iii).~~

11. (currently amended) A eukaryotic cell comprising an exogenous nucleic acid encoding a phytase enzyme, wherein the nucleic acid is operably linked to a transcriptional control sequence and the phytase enzyme (i) is encoded by a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, (ii) is encoded by a nucleic acid comprising a sequence as set forth in SEQ ID NO:1 from nucleotide residue 1 to 1296, ~~[(ii)]~~ (iii) comprises an amino acid sequence as set forth in SEQ ID NO:2, or (iv) comprises an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, ~~or, (iii) comprises an amino acid sequence as set forth in SEQ ID NO:2 or comprises an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, having at least one conservative amino acid substitution, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, (f) a replacement among the aromatic residues Phe, Tyr, or (g) any combination of a, b, c, d, e or f, or (iv) encoding a phytase comprising an enzymatically active fragment of (i), (ii) or (iii).~~

12. (currently amended) A cell comprising an exogenous nucleic acid encoding a phytase enzyme, wherein the nucleic acid is operably linked to a transcriptional control sequence and the phytase enzyme (i) is encoded by a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, (ii) is encoded by a nucleic acid comprising a sequence as set forth in SEQ ID NO:1 from nucleotide residue 1 to 1296, ~~[(ii)]~~ (iii) comprises an amino acid sequence as set forth in SEQ ID NO:2, or (iv) comprises an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, ~~or, (iii) comprises an amino acid sequence as set forth in SEQ ID NO:2 or comprises an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, having at least one conservative amino acid substitution, wherein the conservative amino acid~~

~~substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, (f) a replacement among the aromatic residues Phe, Tyr, or (g) any combination of a, b, c, d, e or f, or (iv) encoding a phytase comprising an enzymatically active fragment of (i), (ii) or (iii).~~

13. (previously presented) A method for making a phytase in a cell comprising:

(a) culturing the cell of claim 12 under conditions wherein the exogenous nucleic acid encoding the phytase enzyme is expressed.

14-15. (canceled)

16. (currently amended) An expression system for making a polypeptide having phytase activity, wherein the phytase activity comprises hydrolyzing inorganic phosphate from phytate or the reverse reaction, comprising a host cell and an exogenous nucleic acid, wherein the host cell is capable of expressing the exogenous nucleic acid, and the exogenous nucleic acid encodes the polypeptide having phytase activity, and the polypeptide having phytase activity (i) is encoded by a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, (ii) is encoded by a nucleic acid comprising a sequence as set forth in SEQ ID NO:1 from nucleotide residue 1 to 1296, [(ii)] (iii) comprises an amino acid sequence as set forth in SEQ ID NO:2, or (iv) comprises an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432,~~or, (iii) comprises an amino acid sequence as set forth in SEQ ID NO:2 or comprises an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432,~~ having at least one conservative amino acid substitution, ~~wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, (f) a replacement among the aromatic residues Phe, Tyr, or (g) any~~

~~combination of a, b, c, d, e or f, or (iv) encoding a phytase comprising an enzymatically active fragment of (i), (ii) or (iii).~~

17. (previously presented) The expression system of claim 16, wherein the exogenous nucleic acid is operably linked to a transcriptional control sequence.

18. (previously presented) The expression system of claim 7 wherein said plant cell is a higher plant cell.

19. (previously presented) The expression system of claim 8 wherein the signal peptide is a secretory signal peptide.

20. (previously presented) The expression system of claim 1 or claim 16, wherein the nucleic acid further comprises a promoter sequence, a secretory sequence, a stabilizing sequence, a targeting sequence or a termination sequence.

21. (currently amended) The expression system of claim 1 or claim 16, wherein the nucleic acid ~~further comprises a vector sequence~~ is contained in a vector.

22. (currently amended) The expression system of claim 21, wherein the vector comprises [[a]] at least a portion of a nucleotide sequence taken from a cloning vector, an expression vector, a bacterial vector, a plasmid, a viral particle, a phage, chromosomal DNA sequences, nonchromosomal DNA sequences, synthetic DNA sequences, a vaccinia vector, an adenovirus vector, a fowl pox virus, a pseudorabies vector or a combination of nucleotide sequences thereof.

23. (currently amended) The vector of claim 2, wherein the vector comprises [[a]] at least a portion of a nucleotide sequence taken from a cloning vector, an expression vector, a bacterial vector, a plasmid, a viral particle, a phage, chromosomal DNA sequences,

nonchromosomal DNA sequences, synthetic DNA sequences, a vaccinia vector, an adenovirus vector, a fowl pox virus, a pseudorabies vector or a combination of nucleotide sequences thereof.

24. (previously presented) The eukaryotic cell of claim 11, wherein the eukaryotic cell is a plant cell.

25. (previously presented) The eukaryotic cell of claim 24, wherein the plant cell is a higher plant cell.

26. (previously presented) The eukaryotic cell of claim 24, wherein the plant cell is a seed cell.

27. (previously presented) The eukaryotic cell of claim 24, wherein the plant cell is an edible flower cell, a cauliflower cell, an artichoke cell, a fruit cell, an apple cell, a banana cell, a berry cell, a currant cell, a cherry cell, a cucumber cell, a grape cell, a lemon cell, a melon cell, a nut cell, an orange cell, a peach cell, a pear cell, a plum cell, a strawberry cell, a tomato cell, a leaf cell, an alfalfa cell, a cabbage cell, an endive cell, a leek cell, a lettuce cell, a spinach cell, a tobacco cell, a root cell, an arrowroot cell, a beet cell, a carrot cell, a cassava cell, a turnip cell, a radish cell, a yam cell, a sweet potato cell, a bean cell, a pea cell, a soybean cell, a wheat cell, a barley cell, a corn cell, a rice cell, a rapeseed cell, a millet cell, a sunflower cell, an oat cell, a tuber cell, a kohlrabi cell or a potato cell.

28. (previously presented) The method of claim 13, further comprising converting the cell into a composition suitable for animal feed.

29. (previously presented) The method of claim 13, wherein the cell is a prokaryotic cell or a eukaryotic cell.

30. (previously presented) The method of claim 29, wherein the eukaryotic cell is a

plant cell.

31. (previously presented) The method of claim 30, wherein the plant cell is a higher plant cell.

32. (previously presented) The method of claim 30, wherein the plant cell is a seed cell.

33. (previously presented) The method of claim 30 wherein the plant cell is an edible flower cell, a cauliflower cell, an artichoke cell, a fruit cell, an apple cell, a banana cell, a berry cell, a currant cell, a cherry cell, a cucumber cell, a grape cell, a lemon cell, a melon cell, a nut cell, an orange cell, a peach cell, a pear cell, a plum cell, a strawberry cell, a tomato cell, a leaf cell, an alfalfa cell, a cabbage cell, an endive cell, a leek cell, a lettuce cell, a spinach cell, a tobacco cell, a root cell, an arrowroot cell, a beet cell, a carrot cell, a cassava cell, a turnip cell, a radish cell, a yam cell, a sweet potato cell, a bean cell, a pea cell, a soybean cell, a wheat cell, a barley cell, a corn cell, a rice cell, a rapeseed cell, a millet cell, a sunflower cell, an oat cell, a tuber cell, a kohlrabi cell or a potato cell.

34. (previously presented) The expression system of claim 16, wherein the phytase activity comprises hydrolyzing inorganic phosphate from phytate.

35. (currently amended) A vector comprising a nucleic acid (i) comprising a nucleotide sequence as set forth in SEQ ID NO:1; (ii) comprising a nucleotide sequence as set forth in SEQ ID NO:1 from nucleotide residue 1 to 1296, ~~[(ii)]~~ (iii) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2; ~~[[or]]~~ (iv) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432; ~~(iii) encoding a phytase comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, wherein the phytase has at least one conservative amino acid substitution, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val,~~

~~Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, or (f) a replacement among the aromatic residues Phe, Tyr; or, [(iii)] (v) comprising a sequence that is the complement of a sequence of (i), (ii) or (iii) (a) a nucleotide sequence as set forth in SEQ ID NO:1; (b) a nucleotide sequence as set forth in SEQ ID NO:1 from nucleotide residues 1 to 1296; (c) the nucleic acid encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2; or (d) the nucleic acid encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432.~~

36. (currently amended) A cell comprising a vector comprising a nucleic acid (i) comprising a nucleotide sequence as set forth in SEQ ID NO:1; (ii) comprising a nucleotide sequence as set forth in SEQ ID NO:1 from nucleotide residue 1 to 1296, [(ii)] (iii) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2; [(or)] (iv) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432; ~~(iii) encoding a phytase comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, wherein the phytase has at least one conservative amino acid substitution, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, or (f) a replacement among the aromatic residues Phe, Tyr; or, [(iii)] (v) comprising a sequence that is the complement of a sequence of (i), (ii) or (iii) (a) a nucleotide sequence as set forth in SEQ ID NO:1; (b) a nucleotide sequence as set forth in SEQ ID NO:1 from nucleotide residues 1 to 1296; (c) the nucleic acid encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2; or (d) the nucleic acid encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432.~~

37. (currently amended) An expression system comprising a nucleic acid (i) comprising

a nucleotide sequence as set forth in SEQ ID NO:1; (ii) comprising a nucleotide sequence as set forth in SEQ ID NO:1 from nucleotide residue 1 to 1296, [(ii)] (iii) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2; [[or]] (iv) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432; (iii) encoding a phytase comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, wherein the phytase has at least one conservative amino acid substitution, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, or (f) a replacement among the aromatic residues Phe, Tyr; or, [(iii)] (v) comprising a sequence that is the complement of a sequence of (i), (ii) or (iii) (a) a nucleotide sequence as set forth in SEQ ID NO:1; (b) a nucleotide sequence as set forth in SEQ ID NO:1 from nucleotide residues 1 to 1296; (c) the nucleic acid encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2; or (d) the nucleic acid encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432.

38. (currently amended) A cloning vector comprising a nucleic acid (i) comprising a nucleotide sequence as set forth in SEQ ID NO:1; (ii) comprising a nucleotide sequence as set forth in SEQ ID NO:1 from nucleotide residue 1 to 1296, [(ii)] (iii) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2; [[or]] (iv) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432; (iii) encoding a phytase comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, wherein the phytase has at least one conservative amino acid substitution, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange

~~of the basic residues Lys and Arg, or (f) a replacement among the aromatic residues Phe, Tyr; or, [(iii)] (v) comprising a sequence that is the complement of a sequence of (i), (ii) or (iii) (a) a nucleotide sequence as set forth in SEQ ID NO:1; (b) a nucleotide sequence as set forth in SEQ ID NO:1 from nucleotide residues 1 to 1296; (c) the nucleic acid encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2; or (d) the nucleic acid encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432.~~

39. (currently amended) An expression vector comprising a nucleic acid (i) comprising a nucleotide sequence as set forth in SEQ ID NO:1; (ii) comprising a nucleotide sequence as set forth in SEQ ID NO:1 from nucleotide residue 1 to 1296, [(ii)] (iii) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2; [[or]] (iv) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432; (iii) encoding a phytase comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, wherein the phytase has at least one conservative amino acid substitution, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, or (f) a replacement among the aromatic residues Phe, Tyr; or, [(iii)] (v) comprising a sequence that is the complement of a sequence of (i), (ii) or (iii) (a) a nucleotide sequence as set forth in SEQ ID NO:1; (b) a nucleotide sequence as set forth in SEQ ID NO:1 from nucleotide residues 1 to 1296; (c) the nucleic acid encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2; or (d) the nucleic acid encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432.

40. (currently amended) A bacterial vector comprising a nucleic acid (i) comprising a nucleotide sequence as set forth in SEQ ID NO:1; (ii) comprising a nucleotide sequence as set forth in SEQ ID NO:1 from nucleotide residue 1 to 1296, [(ii)] (iii) encoding a polypeptide comprising

an amino acid sequence as set forth in SEQ ID NO:2; ~~[[or]]~~ (iv) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432; ~~(iii) encoding a phytase comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, wherein the phytase has at least one conservative amino acid substitution, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, or (f) a replacement among the aromatic residues Phe, Tyr; or, [[(iii)]]~~ (v) comprising a sequence that is the complement of a sequence of (i), (ii) or (iii) (a) a nucleotide sequence as set forth in SEQ ID NO:1; (b) a nucleotide sequence as set forth in SEQ ID NO:1 from nucleotide residues 1 to 1296; (c) the nucleic acid encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2; or (d) the nucleic acid encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432.

41. (currently amended) A plasmid comprising a nucleic acid (i) comprising a nucleotide sequence as set forth in SEQ ID NO:1; (ii) comprising a nucleotide sequence as set forth in SEQ ID NO:1 from nucleotide residue 1 to 1296, [[(ii)]] (iii) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2; ~~[[or]]~~ (iv) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432; ~~(iii) encoding a phytase comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, wherein the phytase has at least one conservative amino acid substitution, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, or (f) a replacement among the aromatic residues Phe, Tyr; or, [[(iii)]]~~ (v) comprising a sequence that is the complement of a sequence of (i), (ii) or (iii) (a) a nucleotide sequence as set forth in SEQ ID NO:1; (b) a nucleotide sequence as set forth in SEQ ID

NO:1 from nucleotide residues 1 to 1296; (c) the nucleic acid encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2; or (d) the nucleic acid encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432.

42. (currently amended) A viral particle comprising a nucleic acid (i) comprising a nucleotide sequence as set forth in SEQ ID NO:1; (ii) comprising a nucleotide sequence as set forth in SEQ ID NO:1 from nucleotide residue 1 to 1296, [(ii)] (iii) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2; [[or]] (iv) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432; (iii) encoding a phytase comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, wherein the phytase has at least one conservative amino acid substitution, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, or (f) a replacement among the aromatic residues Phe, Tyr; or, [(iii)] (v) comprising a sequence that is the complement of a sequence of (i), (ii) or (iii) (a) a nucleotide sequence as set forth in SEQ ID NO:1; (b) a nucleotide sequence as set forth in SEQ ID NO:1 from nucleotide residues 1 to 1296; (c) the nucleic acid encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2; or (d) the nucleic acid encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432.

43. (currently amended) A phage comprising a nucleic acid (i) comprising a nucleotide sequence as set forth in SEQ ID NO:1; (ii) comprising a nucleotide sequence as set forth in SEQ ID NO:1 from nucleotide residue 1 to 1296, [(ii)] (iii) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2; [[or]] (iv) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432; (iii) encoding a phytase comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, wherein the phytase

~~has at least one conservative amino acid substitution, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, or (f) a replacement among the aromatic residues Phe, Tyr; or, [(iii)] (v) comprising a sequence that is the complement of a sequence of (i), (ii) or (iii) (a) a nucleotide sequence as set forth in SEQ ID NO:1; (b) a nucleotide sequence as set forth in SEQ ID NO:1 from nucleotide residues 1 to 1296; (c) the nucleic acid encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2; or (d) the nucleic acid encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432.~~

44 (canceled)

45. (previously presented) A recombinant expression system comprising a nucleic acid encoding a phytase enzyme (i) having the amino acid sequence as set forth in SEQ ID NO:2, or (ii) having an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432.

46. (currently amended) A method for making a phytase in a cell comprising culturing the cell under conditions wherein an exogenous nucleic acid encoding the phytase is expressed, wherein the exogenous nucleic acid comprising a nucleic acid (i) comprising a nucleotide sequence as set forth in SEQ ID NO:1; (ii) comprising a nucleotide sequence as set forth in SEQ ID NO:1 from nucleotide residue 1 to 1296, [(ii)] (iii) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2; [[or]] (iv) encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432; (iii) encoding a phytase comprising an amino acid sequence as set forth in SEQ ID NO:2 or comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432, wherein the phytase has at least one conservative amino acid substitution, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic

~~residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, or (f) a replacement among the aromatic residues Phe, Tyr; or, [(iii)] (v) comprising a sequence that is the complement of a sequence of (i), (ii) or (iii) (a) a nucleotide sequence as set forth in SEQ ID NO:1; (b) a nucleotide sequence as set forth in SEQ ID NO:1 from nucleotide residues 1 to 1296; (c) the nucleic acid encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2; or (d) the nucleic acid encoding a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 from amino acid residue 1 to 432.~~

47. (new) A recombinant expression system comprising a host cell comprising a nucleic acid encoding a phytase comprising an amino acid sequence as set forth in (i) SEQ ID NO:2, or, (ii) SEQ ID NO:2 from amino acid residue 1 to 432, wherein the phytase sequence of (i) or (ii) has at least one conservative amino acid substitution from SEQ ID NO:2, and the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, (f) a replacement among the aromatic residues Phe, Tyr, or (g) any combination of a, b, c, d, e or f;

wherein the nucleic acid is operably linked to a transcriptional control sequence, and the amino acid sequence of the phytase has at least about 50% sequence identity to SEQ ID NO:2.

48. (new) A vector comprising a nucleic acid encoding a phytase comprising an amino acid sequence as set forth in (i) SEQ ID NO:2, or, (ii) SEQ ID NO:2 from amino acid residue 1 to 432, wherein the phytase sequence of (i) or (ii) has at least one conservative amino acid substitution from SEQ ID NO:2, and the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, (f) a replacement among the aromatic residues Phe, Tyr, or (g) any combination of a, b, c, d, e or f;

wherein the nucleic acid is operably linked to a transcriptional control sequence, and the

amino acid sequence of the phytase has at least about 50% sequence identity to SEQ ID NO:2.

49. (new) A recombinant expression system comprising a host cell comprising a nucleic acid encoding an enzymatically active fragment of a phytase, wherein the phytase comprises an amino acid sequence as set forth in (i) SEQ ID NO:2 or (ii) residues 1 to 432 of SEQ ID NO:2, wherein the phytase sequence of (i) or (ii) has at least one conservative amino acid substitution from SEQ ID NO:2, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, (f) a replacement among the aromatic residues Phe, Tyr, or (g) any combination of a, b, c, d, e or f, wherein the nucleic acid is operably linked to a transcriptional control sequence, and the amino acid sequence of the phytase has at least about 50% sequence identity to SEQ ID NO:2.

50. (new) A vector comprising a host cell comprising a nucleic acid encoding an enzymatically active fragment of a phytase, wherein the phytase comprises an amino acid sequence as set forth in (i) SEQ ID NO:2 or (ii) residues 1 to 432 of SEQ ID NO:2, wherein the phytase sequence of (i) or (ii) has at least one conservative amino acid substitution from SEQ ID NO:2, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, (f) a replacement among the aromatic residues Phe, Tyr, or (g) any combination of a, b, c, d, e or f, wherein the nucleic acid is operably linked to a transcriptional control sequence, and the amino acid sequence of the phytase has at least about 50% sequence identity to SEQ ID NO:2.

51. (new) The expression system of claim 47 or claim 49, wherein the transcriptional control sequence comprises a constitutive promoter or a tissue-specific promoter.

52. (new) The vector of claim 48 or claim 50, wherein the transcriptional control sequence comprises a constitutive promoter or a tissue-specific promoter.

53. (new) The expression system of claim 47 or claim 49, wherein the host cell is a prokaryotic cell or a eukaryotic cell.

54. (new) The expression system of claim 47 or claim 49, wherein the host cell is a plant cell, or optionally is a higher plant cell.

55. (new) The expression system of claim 47 or claim 49, wherein the nucleic acid further comprises a sequence encoding a signal peptide or a transit peptide, a promoter sequence, a secretory sequence, a stabilizing sequence, a targeting sequence or a termination sequence and optionally the signal peptide comprises a pathogenesis-related (PR) protein PR-S signal peptide from tobacco, or optionally the signal peptide is a secretory signal peptide.

56. (new) The vector of claim 48 or claim 50, wherein the nucleic acid further comprises a sequence encoding a signal peptide or a transit peptide, a promoter sequence, a secretory sequence, a stabilizing sequence, a targeting sequence or a termination sequence, and optionally the signal peptide comprises a pathogenesis-related (PR) protein PR-S signal peptide from tobacco, or optionally the signal peptide is a secretory signal peptide.

57. (new) The expression system of claim 47 or claim 49, wherein the phytase activity comprises hydrolyzing inorganic phosphate from phytate or the reverse reaction.

58. (new) The vector of claim 48 or claim 50, wherein the phytase activity comprises hydrolyzing inorganic phosphate from phytate or the reverse reaction.

59. (new) The vector of claim 48 or claim 50, wherein the vector comprises at least a portion of a nucleotide sequence taken from a cloning vector, an expression vector, a bacterial

vector, a plasmid, a viral particle, a phage, chromosomal DNA, nonchromosomal DNA, synthetic DNA, a vaccinia vector, an adenovirus vector, a fowl pox virus, a pseudorabies vector or a combination of nucleotide sequences thereof.

60. (new) The vector of claim 48 or claim 50, wherein the vector comprises at least a portion of a nucleotide sequence taken from a cloning vector, an expression vector, a bacterial vector, a plasmid, a viral particle, a phage, chromosomal DNA, nonchromosomal DNA, synthetic DNA, a vaccinia vector, an adenovirus vector, a fowl pox virus, a pseudorabies vector or a combination of nucleotide sequences thereof.

61. (new) A cell comprising an exogenous nucleic acid encoding a phytase comprising an amino acid sequence as set forth in (i) SEQ ID NO:2, or, (ii) SEQ ID NO:2 from amino acid residue 1 to 432, wherein the phytase sequence of (i) or (ii) has at least one conservative amino acid substitution from SEQ ID NO:2, and the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, (f) a replacement among the aromatic residues Phe, Tyr, or (g) any combination of a, b, c, d, e or f;

wherein the nucleic acid is operably linked to a transcriptional control sequence, and the amino acid sequence of the phytase has at least about 50% sequence identity to SEQ ID NO:2.

62. (new) A cell comprising an exogenous nucleic acid encoding an enzymatically active fragment of a phytase, wherein the phytase comprises an amino acid sequence as set forth in (i) SEQ ID NO:2 or (ii) residues 1 to 432 of SEQ ID NO:2, wherein the phytase sequence of (i) or (ii) has at least one conservative amino acid substitution from SEQ ID NO:2, wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues

Asn and Gln, (e) an exchange of the basic residues Lys and Arg, (f) a replacement among the aromatic residues Phe, Tyr, or (g) any combination of a, b, c, d, e or f,

wherein the nucleic acid is operably linked to a transcriptional control sequence, and the amino acid sequence of the phytase has at least about 50% sequence identity to SEQ ID NO:2.

63. (new) The cell of claim 61 or claim 62, wherein the cell is a prokaryotic cell or a eukaryotic cell.

64. (new) The cell of claim 61 or claim 62, wherein the cell is a plant cell or a seed cell.

65. (new) The cell of claim 64, wherein the plant cell is an edible flower cell, a cauliflower cell, an artichoke cell, a fruit cell, an apple cell, a banana cell, a berry cell, a currant cell, a cherry cell, a cucumber cell, a grape cell, a lemon cell, a melon cell, a nut cell, an orange cell, a peach cell, a pear cell, a plum cell, a strawberry cell, a tomato cell, a leaf cell, an alfalfa cell, a cabbage cell, an endive cell, a leek cell, a lettuce cell, a spinach cell, a tobacco cell, a root cell, an arrowroot cell, a beet cell, a carrot cell, a cassava cell, a turnip cell, a radish cell, a yam cell, a sweet potato cell, a bean cell, a pea cell, a soybean cell, a wheat cell, a barley cell, a corn cell, a rice cell, a rapeseed cell, a millet cell, a sunflower cell, an oat cell, a tuber cell, a kohlrabi cell or a potato cell.

66. (new) A method for making a phytase in a cell comprising culturing the cell of claim 61 or claim 62 under conditions wherein the exogenous nucleic acid encoding the phytase is expressed.

67. (new) The method of claim 66, further comprising converting the cell into a composition suitable for animal feed.

68. (new) The method of claim 66, wherein the cell is a prokaryotic cell or a eukaryotic cell, and optionally the cell is a plant cell or a seed cell.

69. (new) The method of claim 68, wherein the plant cell is a higher plant cell.

70. (new) The method of claim 68, wherein the plant cell is an edible flower cell, a cauliflower cell, an artichoke cell, a fruit cell, an apple cell, a banana cell, a berry cell, a currant cell, a cherry cell, a cucumber cell, a grape cell, a lemon cell, a melon cell, a nut cell, an orange cell, a peach cell, a pear cell, a plum cell, a strawberry cell, a tomato cell, a leaf cell, an alfalfa cell, a cabbage cell, an endive cell, a leek cell, a lettuce cell, a spinach cell, a tobacco cell, a root cell, an arrowroot cell, a beet cell, a carrot cell, a cassava cell, a turnip cell, a radish cell, a yam cell, a sweet potato cell, a bean cell, a pea cell, a soybean cell, a wheat cell, a barley cell, a corn cell, a rice cell, a rapeseed cell, a millet cell, a sunflower cell, an oat cell, a tuber cell, a kohlrabi cell or a potato cell.

71. (new) The expression system of claim 47 or claim 49, wherein the amino acid sequence of the phytase has at least about 70% sequence identity to SEQ ID NO:2.

72. (new) The expression system of claim 71, wherein the phytase has at least about 80% sequence identity to SEQ ID NO:2.

73. (new) The expression system of claim 72, wherein the phytase has at least about 90% sequence identity to SEQ ID NO:2.

74. (new) The expression system of claim 73, wherein the phytase has at least about 95% sequence identity to SEQ ID NO:2.

75. (new) The vector of claim 48 or claim 50, wherein the amino acid sequence of the phytase has at least about 70% sequence identity to SEQ ID NO:2.

76. (new) The cell of claim 61 or claim 62, wherein the amino acid sequence of the phytase has at least about 70% sequence identity to SEQ ID NO:2.